



Characteristics of synonymous codon usage bias in the beginning region of West Nile virus

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ABSTRACT. Adaptation in the overall codon usage pattern of West Nile virus (WNV) to that of two hosts was estimated based on the synonymous codon usage value (RSCU). Synonymous codon usage biases for the beginning coding sequence of this virus were also analyzed by calculating the usage fluctuation for each synonymous codon along the target region (the first 270 codon sites of the whole coding sequence of WNV). Adaptation of WNV to *Anopheles gambiae* regarding the overall codon usage revealed a mixture of synonymous codon usage patterns between this virus and its vector. Regarding the adaptation of WNV to its dead-end host and codon usage, although a mixture of overall codon usage patterns exists, the number of codons with reversed tendency codon usage is lower than that between the virus and its vector. In addition, some codons with low RSCU values for this virus are highly selected in the beginning translation region of WNV, while codons with low RSCU values in this region tend to pair with tRNAs present in low abundance in the host, suggesting that highly selected

codons in a specific region in the beginning region of WNV are, to some degree, influenced by the corresponding low tRNA abundance of hosts to regulate the translation speed of the WNV polyprotein.

Key words: West Nile virus; Codon usage; tRNA abundance; Beginning translation region